



SEQUENCE LISTING

<110> Hilton, Douglas J.
Nicola, Nicos A.
Farley, Alison
Wilson, Tracy
Zhang, Jian-Guo
Alexander, Warren
Rakar, Steven
Fabri, Louis
Kojima, Tetsuo
Maeda, Masatsugu
Kikuchi, Yasufumi
Nash, Andrew

<120> A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

<130> DAVIES COLLISON CAVE (CIP)

<140> 09/037,657
<141> 1998-03-10

<150> 08/928,720
<151> 1997-09-11

<160> 58

<170> PatentIn Ver. 2.0

<210> 1
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<213> Unknown

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<223> Unsure at position 3

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<212> DNA
<213> Artificial Sequence

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<400> 2
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<210> 3
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<210> 8
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<210> 9
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<400> 10
 ggaggtgtta aggaggcg 18

<210> 11
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:2120 probe

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18

<210> 12

<211> 1629

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<222> (124)..(1362)

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<223> Description of Unknown Organism:Murine NR6.1

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ccccgcagac tcgccccgc ccataaccgg cgttgcagtc accgcccgtt gcgcgccacc 120

ccc	atg	ccc	gcg	ggt	cgc	ccg	ggc	ccc	gtc	gcc	caa	tcc	gcg	cgg	cgg	168
	Met	Pro	Ala	Gly	Arg	Pro	Gly	Pro	Val	Ala	Gln	Ser	Ala	Arg	Arg	
	1				5					10					15	

ccg	ccg	cgg	ccg	ctg	tcc	tcg	ctg	tgg	tcg	cct	ctg	ttg	ctc	tgt	gtc	216
Pro	Pro	Arg	Pro	Leu	Ser	Ser	Leu	Trp	Ser	Pro	Leu	Leu	Leu	Cys	Val	
				20					25					30		

ctc	ggg	gtg	cct	cgg	ggc	gga	tcg	gga	gcc	cac	aca	gct	gta	atc	agc	264
Leu	Gly	Val	Pro	Arg	Gly	Gly	Ser	Gly	Ala	His	Thr	Ala	Val	Ile	Ser	
			35					40					45			

ccc	cag	gac	ccc	acc	ctt	ctc	atc	ggc	tcc	tcc	ctg	caa	gct	acc	tgc	312
Pro	Gln	Asp	Pro	Thr	Leu	Leu	Ile	Gly	Ser	Ser	Leu	Gln	Ala	Thr	Cys	
		50					55					60				

tct	ata	cat	gga	gac	aca	cct	ggg	gcc	acc	gct	gag	ggg	ctc	tac	tgg	360
Ser	Ile	His	Gly	Asp	Thr	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	Trp	
	65					70					75					

acc	ctc	aat	ggt	cgc	cgc	ctg	ccc	tct	gag	ctg	tcc	cgc	ctc	ctt	aac	408
Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	
	80				85					90					95	

acc	tcc	acc	ctg	gcc	ctg	gcc	ctg	gct	aac	ctt	aat	ggg	tcc	agg	cag	456
Thr	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	
				100					105					110		

cag	tca	gga	gac	aat	ctg	gtg	tgt	cac	gcc	cga	gac	ggc	agc	att	ctg	504
Gln	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	
			115					120					125			

gct	ggc	tcc	tgc	ctc	tat	gtt	ggc	ttg	ccc	cct	gag	aag	ccc	ttt	aac	552
Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	
		130					135					140				

atc	agc	tgc	tgg	tcc	cgg	aac	atg	aag	gat	ctc	acg	tgc	cgc	tgg	aca	600
Ile	Ser	Cys	Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	

145				150				155								
ccg Pro 160	ggt Gly	gca Ala	cac His	ggg Gly 165	gag Glu 165	aca Thr	ttc Phe	tta Leu	cat His 170	acc Thr 170	aac Asn	tac Tyr	tcc Ser	ctc Leu	aag Lys 175	648
tac Tyr	aag Lys	ctg Leu	agg Arg	tgg Trp 180	tac Tyr	ggt Gly	cag Gln	gat Asp	aac Asn 185	aca Thr	tgt Cys	gag Glu	gag Glu	tac Tyr 190	cac His	696
act Thr	gtg Val	ggc Gly	cct Pro 195	cac His	tca Ser	tgc Cys	cat His	atc Ile 200	ccc Pro	aag Lys	gac Asp	ctg Leu	gcc Ala 205	ctc Leu	ttc Phe	744
act Thr	ccc Pro	tat Tyr 210	gag Glu	atc Ile	tgg Trp	gtg Val	gaa Glu 215	gcc Ala	acc Thr	aat Asn	cgc Arg	cta Leu 220	ggc Gly	tca Ser	gca Ala	792
aga Arg	tct Ser 225	gat Asp	gtc Val	ctc Leu	aca Thr	ctg Leu 230	gat Asp	gtc Val	ctg Leu	gac Asp	gtg Val 235	gtg Val	acc Thr	acg Thr	gac Asp	840
ccc Pro 240	cca Pro	ccc Pro	gac Asp	gtg Val 245	cac His	gtg Val	agc Ser	cgc Arg	gtt Val	ggg Gly 250	ggc Gly	ctg Leu	gag Glu	gac Asp	cag Gln 255	888
ctg Leu	agt Ser	gtg Val	cgc Arg	tgg Trp 260	gtc Val	tca Ser	cca Pro	cca Pro	gct Ala 265	ctc Leu	aag Lys	gat Asp	ttc Phe	ctc Leu 270	ttc Phe	936
caa Gln	gcc Ala	aag Lys	tac Tyr 275	cag Gln	atc Ile	cgc Arg	tac Tyr	cgc Arg 280	gtg Val	gag Glu	gac Asp	agc Ser	gtg Val 285	gac Asp	tgg Trp	984
aag Lys	gtg Val	gtg Val	gat Asp	gac Asp	gtc Val	agc Ser	aac Asn 295	cag Gln	acc Thr	tcc Ser	tgc Cys	cgt Arg 300	ctc Leu	gcg Ala	ggc Gly	1032
ctg Leu	aag Lys 305	ccc Pro	ggc Gly	acc Thr	gtt Val	tac Tyr 310	ttc Phe	gtc Val	caa Gln	gtg Val	cgt Arg 315	tgt Cys	aac Asn	cca Pro	ttc Phe	1080
ggg Gly 320	atc Ile	tat Tyr	ggg Gly	tgc Ser	aaa Lys 325	aag Lys	gcg Ala	gga Gly	atc Ile	tgg Trp 330	agc Ser	gag Glu	tgg Trp	agc Ser	cac His 335	1128
ccc Pro	acc Thr	gct Ala	gcc Ala	tcc Ser 340	acc Thr	cct Pro	cga Arg	agt Ser	gag Glu 345	cgc Arg	ccg Pro	ggc Gly	ccg Pro	ggc Gly 350	ggc Gly	1176
ggg Gly	gtg Val	tgc Cys	gag Glu 355	ccg Pro	cgg Arg	ggc Gly	ggc Gly	gag Glu 360	ccc Pro	agc Ser	tgc Ser	ggc Gly	ccg Pro	gtg Val 365	cgg Arg	1224
cgc Arg	gag Glu	ctc Leu 370	aag Lys	cag Gln	ttc Phe	ctc Leu	ggc Gly 375	tgg Trp	ctc Leu	aag Lys	aag Lys	cac His 380	gca Ala	tac Tyr	tgc Cys	1272
tgc Ser	aac Asn 385	ctt Leu	agt Ser	ttc Phe	cgc Arg	ctg Leu 390	tac Tyr	gac Asp	cag Gln	tgg Trp	cgt Arg 395	gct Ala	tgg Trp	atg Met	cag Gln	1320
aag Lys	tca Val	cac His	aag Lys	acc Thr	cga Arg	aac Asn	cag Gln	gtc Val	ctg Leu	ccg Pro	gct Ala	aaa Lys	ctc Leu			1362

Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
400 405 410

taaggatagg ccattctcct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422
ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482
ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaagggttg 1542
ggtattgcag ggcctcccaa caatctcttt aaataaataa aggagttggt caggtaaaaa 1602
aaaaaaaaa aaaaaaaaaa aaaaaaa 1629

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<211> 413
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6.1

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Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
20 25 30
Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45
Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
50 55 60
Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65 70 75 80
Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95
Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110
Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125
Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
130 135 140
Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160
Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175
Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190
Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205
Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
 225 230 235 240
 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
 245 250 255
 Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
 260 265 270
 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
 275 280 285
 Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
 290 295 300
 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
 305 310 315 320
 Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
 325 330 335
 Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
 340 345 350
 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
 355 360 365
 Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
 370 375 380
 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
 385 390 395 400
 Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
 405 410

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 <213> Unknown

<220>
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 <222> (125)..(1399)

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 ccccgagac tcgccccgc ccataaccgg cggtgcagtc accgcccgtt gcgcgccacc 120
 ccca atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 169
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
 1 5 10 15
 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 217
 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
 20 25 30

ctc Leu	ggg Gly	gtg Val	cct Pro 35	cgg Arg	ggc Gly	gga Gly	tcg Ser	gga Gly 40	gcc Ala	cac His	aca Thr	gct Ala	gta Val 45	atc Ile	agc Ser	265
ccc Pro	cag Gln	gac Asp 50	ccc Pro	acc Thr	ctt Leu	ctc Leu	atc Ile 55	ggc Gly	tcc Ser	tcc Ser	ctg Leu	caa Gln 60	gct Ala	acc Thr	tgc Cys	313
tct Ser	ata Ile 65	cat His	gga Gly	gac Asp	aca Thr	cct Pro 70	ggg Gly	gcc Ala	acc Thr	gct Ala	gag Glu 75	ggg Gly	ctc Leu	tac Tyr	tgg Trp	361
acc Thr 80	ctc Leu	aat Asn	ggg Gly	cgc Arg	cgc Arg 85	ctg Leu	ccc Pro	tct Ser	gag Glu 90	ctg Leu	tcc Ser	cgc Arg	ctc Leu	ctt Leu	aac Asn 95	409
acc Thr	tcc Ser	acc Thr	ctg Leu	gcc Ala 100	ctg Leu	gcc Ala	ctg Leu	gct Ala	aac Asn 105	ctt Leu	aat Asn	ggg Gly	tcc Ser	agg Arg 110	cag Gln	457
cag Gln	tca Ser	gga Gly	gac Asp 115	aat Asn	ctg Leu	gtg Val	tgt Cys	cac His 120	gcc Ala	cga Arg	gac Asp	ggc Gly	agc Ser 125	att Ile	ctg Leu	505
gct Ala	ggc Gly	tcc Ser 130	tgc Cys	ctc Leu	tat Tyr	gtt Val	ggc Gly 135	ttg Leu	ccc Pro	cct Pro	gag Glu	aag Lys 140	ccc Pro	ttt Phe	aac Asn	553
atc Ile	agc Ser 145	tgc Cys	tgg Trp	tcc Ser	cgg Arg	aac Asn 150	atg Met	aag Lys	gat Asp	ctc Leu	acg Thr 155	tgc Cys	cgc Arg	tgg Trp	aca Thr	601
ccg Pro 160	ggg Gly	gca Ala	cac His	ggg Gly	gag Glu 165	aca Thr	ttc Phe	tta Leu	cat His	acc Thr 170	aac Asn	tac Tyr	tcc Ser	ctc Leu	aag Lys 175	649
tac Tyr	aag Lys	ctg Leu	agg Arg	tgg Trp 180	tac Tyr	ggg Gly	cag Gln	gat Asp	aac Asn 185	aca Thr	tgt Cys	gag Glu	gag Glu	tac Tyr 190	cac His	697
act Thr	gtg Val	ggc Gly	cct Pro 195	cac His	tca Ser	tgc Cys	cat His	atc Ile 200	ccc Pro	aag Lys	gac Asp	ctg Leu	gcc Ala 205	ctc Leu	ttc Phe	745
act Thr	ccc Pro	tat Tyr 210	gag Glu	atc Ile	tgg Trp	gtg Val	gaa Glu 215	gcc Ala	acc Thr	aat Asn	cgc Arg	cta Leu 220	ggc Gly	tca Ser	gca Ala	793
aga Arg	tct Ser 225	gat Asp	gtc Val	ctc Leu	aca Thr	ctg Leu 230	gat Asp	gtc Val	ctg Leu	gac Asp	gtg Val 235	gtg Val	acc Thr	acg Thr	gac Asp	841
ccc Pro 240	cca Pro	ccc Pro	gac Asp	gtg Val	cac His 245	gtg Val	agc Ser	cgc Arg	gtt Val	ggg Gly 250	ggc Gly	ctg Leu	gag Glu	gac Asp	cag Gln 255	889
ctg Leu	agt Ser	gtg Val	cgc Arg	tgg Trp 260	gtc Val	tca Ser	cca Pro	cca Pro	gct Ala 265	ctc Leu	aag Lys	gat Asp	ttc Phe	ctc Leu 270	ttc Phe	937
caa Gln	gcc Ala	aag Lys	tac Tyr 275	cag Gln	atc Ile	cgc Arg	tac Tyr	cgc Arg 280	gtg Val	gag Glu	gac Asp	agc Ser	gtg Val 285	gac Asp	tgg Trp	985

aag	gtg	gtg	gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	1033
Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	
		290					295					300				
ctg	aag	ccc	ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	1081
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	
	305					310					315					
ggg	atc	tat	ggg	tcg	aaa	aag	gcg	gga	atc	tgg	agc	gag	tgg	agc	cac	1129
Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	
320					325					330					335	
ccc	acc	gct	gcc	tcc	acc	cct	cga	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	1177
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly	
				340					345					350		
ggg	gtg	tgc	gag	ccg	cgg	ggc	ggc	gag	ccc	agc	tcg	ggc	ccg	gtg	cgg	1225
Gly	Val	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	
			355					360					365			
cgc	gag	ctc	aag	cag	ttc	ctc	ggc	tgg	ctc	aag	aag	cac	gca	tac	tgc	1273
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	
		370					375					380				
tcg	aac	ctt	agt	ttc	cgc	ctg	tac	gac	cag	tgg	cgt	gct	tgg	atg	cag	1321
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	
	385					390					395					
aag	tca	cac	aag	acc	cga	aac	cag	gac	gag	ggg	atc	ctg	cct	tcg	ggc	1369
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	Asp	Glu	Gly	Ile	Leu	Pro	Ser	Gly	
400					405					410					415	
aga	cgg	ggt	gcg	gcg	aga	ggt	cct	gcc	ggt	taaactctaa	ggataggcca					1419
Arg	Arg	Gly	Ala	Ala	Arg	Gly	Pro	Ala	Gly							
				420					425							
tcctcctgct	gggtcagacc	tgagggtc	cctgaattgg	agcccctctg	taccatctgg											1479
gcaacaaaga	aacctaccag	aggctggggc	acaatgagct	cccacaacca	cagctttggt											1539
ccacatgatg	gtcacacttg	gatatacccc	agtgtgggta	aggttggggg	attgcagggc											1599
ctcccaacaa	tctctttaa	taaataaagg	agttgttcag	gtaaaaaaaa	aaaaaaaaaa											1659
aaaaaaaaaa	aaaa															1673

<210> 15
 <211> 425
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Murine NR6.2

<400> 15
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 20 25 30
 Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
 50 55 60
 Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
 65 70 75 80
 Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
 85 90 95
 Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
 100 105 110
 Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
 115 120 125
 Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
 130 135 140
 Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
 145 150 155 160
 Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
 165 170 175
 Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
 180 185 190
 Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
 195 200 205
 Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
 210 215 220
 Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
 225 230 235 240
 Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
 245 250 255
 Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
 260 265 270
 Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
 275 280 285
 Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
 290 295 300
 Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
 305 310 315 320
 Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
 325 330 335
 Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
 340 345 350
 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
 355 360 365
 Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
 370 375 380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
 385 390 395 400
 Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
 405 410 415
 Arg Gly Ala Ala Arg Gly Pro Ala Gly
 420 425

<210> 16
 <211> 938
 <212> DNA
 <213> Unknown

<220>
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 <222> (1)..(465)

<220>
 <223> Description of Unknown Organism: Murine NR6.3

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 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
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 ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac ccc acc gct 96
 Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
 20 25 30
 gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc ggg gtg tgc 144
 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
 35 40 45
 gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg cgc gag ctc 192
 Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
 50 55 60
 aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc tcg aac ctt 240
 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65 70 75 80
 agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag aag tca cac 288
 Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
 85 90 95
 aag acc cga aac cag gta gga aag ttg ggg gag gct tgc gtg ggg ggt 336
 Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
 100 105 110
 aaa gga gca gag gaa gag aga gac ccg ggt gag cag cct cca caa cac 384
 Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
 115 120 125
 cgc act ctt ctt tcc aag cac agg acg agg gga tcc tgc cct cgg gca 432
 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
 130 135 140
 gac ggg gtg cgg cga gag gta agg ggg tct ggg tgagtggggc ctacagcagt 485
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
 145 150 155
 11

ctagatgagg ccctttcccc tccttcggtg ttgctcaaag ggatctctta gtgctcattt 545
 caccactgc aaagagcccc aggttttact gcatcatcaa gttgctgaag ggtccaggct 605
 taatgtggcc tcttttctgc cctcaggctc tgccggctaa actctaagga taggccatcc 665
 tcctgctggg tcagacctgg aggctcacct gaattggagc ccctctgtac ctatctgggc 725
 aacaaagaaa cctaccatga ggctggggca caatgagctc ccacaaccac agctttgggc 785
 cacatgatgg tcacacttgg atatacccca gtgtgggtaa gggtggggta ttgcagggcc 845
 tccaacaat ctctttaaat aaataaagga gttgttcagg taaaaaaaaa aaaaaaaaaa 905
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 938

<210> 17
 <211> 155
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Murine NR6.3

<400> 17
 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 1 5 10 15
 Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
 20 25 30
 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
 35 40 45
 Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
 50 55 60
 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65 70 75 80
 Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
 85 90 95
 Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
 100 105 110
 Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
 115 120 125
 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
 130 135 140
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
 145 150 155

<210> 18
 <211> 834
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(834)

<220>
 <223> Description of Artificial Sequence: Nucleotide
 sequence of products generated by 5' RACE of brain
 cDNA using NR6 specific primers

<400> 18
 ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc tct ata cat 48
 Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
 1 5 10 15

gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg acc ctc aat 96
 Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
 20 25 30

ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac acc tcc acc 144
 Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
 35 40 45

ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag cag tca gga 192
 Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
 50 55 60

gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg gct ggc tcc 240
 Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
 65 70 75 80

tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac atc agc tgc 288
 Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
 85 90 95

tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca ccg ggt gca 336
 Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
 100 105 110

cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag tac aag ctg 384
 His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
 115 120 125

agg tgg tac ggt cag gat aac aca tgt gag gag tac cac act gtg ggg 432
 Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
 130 135 140

ccc cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc act ccc tat 480
 Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
 145 150 155 160

gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca aga tct gat 528
 Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
 165 170 175

gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac ccc cca ccc 576
 Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
 180 185 190

gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag ctg agt gtg 624
 Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
 195 200 205

cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc caa gcc aag 672
 13

Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys		
210						215					220						
tac	cag	atc	cgc	tac	cgc	gtg	gag	gac	agc	gtg	gac	tgg	aag	gtg	gtg	720	
Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val	240	
225					230					235							
gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	ctg	aag	ccc	768	
Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro	255	
				245					250								
ggc	acc	gtt	tac	ttc	gtc	caa	gtg	cgt	tgt	aac	cca	ttc	ggg	atc	tat	816	
Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr	270	
			260					265									
ggg	tcg	aaa	aag	gcg	gga											834	
Gly	Ser	Lys	Lys	Ala	Gly												
		275															

<210> 19
 <211> 278
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Haemopoietin receptor

<400> 19
 Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
 1 5 10 15
 Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
 20 25 30
 Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
 35 40 45
 Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
 50 55 60
 Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
 65 70 75 80
 Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
 85 90 95
 Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
 100 105 110
 His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
 115 120 125
 Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
 130 135 140
 Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
 145 150 155 160
 Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
 165 170 175
 Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
 180 185 190

Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
 195 200 205
 Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
 210 215 220
 Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
 225 230 235 240
 Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
 245 250 255
 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 260 265 270
 Gly Ser Lys Lys Ala Gly
 275

<210> 20
 <211> 143
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (105)..(143)

<220>
 <223> Description of Artificial Sequence:Nucleotide
 sequence unique to 5' RACE of brain cDNA

<400> 20
 ggcatgaagg cttagggtgg ggatcggtag gacccatgca cccagagaaa gggactggtg 60
 gcaactttca aactctctgg ggaaggaaga agggctgaaa gagg atg aac ggg ctc 116
 Met Asn Gly Leu
 1
 aga cac agc tgt aat cag ccc cca gga 143
 Arg His Ser Cys Asn Gln Pro Pro Gly
 5 10

<210> 21
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Amino Acid Sequence encoded by Nucleotide
 sequence unique to 5' RACE of brain cDNA

<400> 21
 Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
 1 5 10

<210> 22
 <211> 1930
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown Organism: Murine NR6

<400> 22

ggcacgagct tcgctgtccg cgcccagtga cgcgcggtgcg gacccgagcc ccaatctgca 60
ccccgcagac tcgccccgcg cccataaccgg cgttgcagtc accgcccgtt gcgcgccacc 120
cccaatgccc gcgggtcgcc cgggccccgt cgcccaatcc gcgcggcggc cgccgcggcc 180
gctgtcctcg ctgtggtcgc ctctgttgct ctgtgtcctc ggggtgcctc ggggcggatc 240
gggagccac acagctgtaa tcagccccc ggacccacc cttctcatcg gtcctccct 300
gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg ggctctactg 360
gacctcaat ggtcgccgcc tgccctctga gctgtccgc ctcttaaca cctccaccct 420
ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca atctgggtgtg 480
tcacgcccga gacggcagca ttctggctgg ctctgcctc tatgttggt tgccccctga 540
gaagcccttt aacatcagct gctggtcccg gaacatgaag gatctcacgt gccgctggac 600
accgggtgca cacggggaga cattcttaca taccaactac tccctcaagt acaagctgag 660
gtggtacggt caggataaca catgtgagga gtaccacact gtgggccctc actcatgcca 720
tatccccaag gacctggccc tcttactcc ctatgagatc tgggtggaag ccaccaatcg 780
cctaggctca gcaagatctg atgtcctcac actggatgtc ctggacgtgg tgaccacgga 840
ccccccacc gacgtgcacg tgagccgcgt tgggggcctg gaggaccagc tgagtgtgcg 900
ctgggtctca ccaccagctc tcaaggattt cctcttccaa gccaagtacc agatccgcta 960
ccgcgtggag gacagcgtgg actggaaggt ggtggatgac gtcagcaacc agacctcctg 1020
ccgtctcgcg ggcctgaagc ccggcaccgt ttacttcgtc caagtgcgtt gtaaccatt 1080
cgggatctat gggctgaaaa aggcgggaat ctggagcgag tggagccacc ccaccgctgc 1140
ctccaccct cgaagtgagc gcccgggccc gggcgggcgg gtgtgcgagc cgcggggcgg 1200
cgagcccagc tcgggcccgg tcgggcgcga gctcaagcag ttcctcggt ggctcaagaa 1260
gcacgcatac tgctcgaacc ttagtttccg cctgtacgac cagtggcgtg cttggatgca 1320
gaagtcacac aagacccgaa accaggtagg aaagtgggg gaggcttgcg tggggggtaa 1380
aggagcagag gaagagagag acccggtga gcagcctca caacaccga ctcttctttc 1440
caagcacagg acgaggggat cctgccctcg ggcagacggg gtgcggcgag aggtaagggg 1500
gtctgggtga gtggggccta cagcagtcta gatgaggccc tttcccctcc ttcggtgttg 1560
ctcaaagga tctcttagtg ctattttcac cactgcaaa gagccccagg ttttactgca 1620
tcataagtt gctgaagggt ccaggcttaa tgtggcctct tttctgccct caggctctgc 1680
cggctaaact ctaaggatag gccatcctcc tgctgggtca gacctggagg ctcacctgaa 1740
ttggagcccc tctgtaccta tctgggcaac aaagaaacct accatgaggc tggggcacia 1800

tgagctccca caaccacagc tttggtccac atgatggtca cacttggata taccccagtg 1860
 tgggtaaggt tggggtattg cagggcctcc caacaatctc tttaaataaa taaaggagtt 1920
 gttcaggtaa 1930

<210> 23
 <211> 560
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR product for
 human NR6

<400> 23
 tccaggcagc ggtcggggga caacctcgtg tgccacgccc gtgacggcag catcctggct 60
 ggctcctgcc tctatgttgg cctgccccca gagaaaccg tcaacatcag ctgctggtcc 120
 aagaacatga aggacttgac ctgccgctgg acgccagggg cccacgggga gaccttcctc 180
 cacaccaact actccctcaa gtacaagctt aggtggtatg gccaggacaa cacatgtgag 240
 gagtaccaca cagtggggcc ccactcctgc cacatcccca aggacctggc tctctttacg 300
 ccctatgaga tctgggtgga ggccaccaac cgcttgggct ctgcccgtc cgatgtactc 360
 acgctggata tcctggatgt ggtgaccacg gacccccgc ccgacgtgca cgtgagccgc 420
 gtcgggggccc tggaggacca gctgagcgtg cgctgggtgt cgccaccgc cctcaaggat 480
 ttcctttttc aagccaaata ccagatccgc taccgagtgg aggacagtgt ggaatggaag 540
 gtggtggacg atgtgagcaa 560

<210> 24
 <211> 1391
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)..(1050)

<220>
 <223> Description of Unknown Organism:Nucleotide
 sequence of clone HFK-66 encoding human NR6

<400> 24
 acc ctc aac ggg cgc cgc ctg ccc cct gag ctc tcc cgt gta ctc aac 48
 Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1 5 10 15
 gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat ggg tcc agg cag 96
 Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 20 25 30
 cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac ggc agc atc ctg 144
 Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 35 40 45

gct Ala	ggc Gly 50	tcc Ser	tgc Cys	ctc Leu	tat Tyr	gtt Val 55	ggc Gly	ctg Leu	ccc Pro	cca Pro	gag Glu 60	aaa Lys	ccc Pro	gtc Val	aac Asn	192
atc Ile 65	agc Ser	tgc Cys	tgg Trp	tcc Ser	aag Lys 70	aac Asn	atg Met	aag Lys	gac Asp	ttg Leu 75	acc Thr	tgc Cys	cgc Arg	tgg Trp	acg Thr 80	240
cca Pro	ggg Gly	gcc Ala	cac His	ggg Gly 85	gag Glu	acc Thr	ttc Phe	ctc Leu	cac His 90	acc Thr	aac Asn	tac Tyr	tcc Ser	ctc Leu 95	aag Lys	288
tac Tyr	aag Lys	ctt Leu	agg Arg 100	tgg Trp	tat Tyr	ggc Gly	cag Gln	gac Asp 105	aac Asn	aca Thr	tgt Cys	gag Glu 110	gag Glu 110	tac Tyr	cac His	336
aca Thr	gtg Val	ggg Gly 115	ccc Pro	cac His	tcc Ser	tgc Cys	cac His 120	atc Ile	ccc Pro	aag Lys	gac Asp	ctg Leu 125	gct Ala	ctc Leu	ttt Phe	384
acg Thr	ccc Pro 130	tat Tyr	gag Glu	atc Ile	tgg Trp	gtg Val 135	gag Glu	gcc Ala	acc Thr	aac Asn	cgc Arg 140	ctg Leu	ggc Gly	tct Ser	gcc Ala	432
cgc Arg 145	tcc Ser	gat Asp	gta Val	ctc Leu	acg Thr 150	ctg Leu	gat Asp	atc Ile	ctg Leu	gat Asp 155	gtg Val	gtg Val	acc Thr	acg Thr	gac Asp 160	480
ccc Pro	ccg Pro	ccc Pro	gac Asp	gtg Val 165	cac His	gtg Val	agc Ser	cgc Arg	gtc Val 170	ggg Gly	ggc Gly	ctg Leu	gag Glu	gac Asp 175	cag Gln	528
ctg Leu	agc Ser	gtg Val	cgc Arg 180	tgg Trp	gtg Val	tcg Ser	cca Pro	ccc Pro 185	gcc Ala	ctc Leu	aag Lys	gat Asp	ttc Phe 190	ctc Leu	ttt Phe	576
caa Gln	gcc Ala	aaa Lys 195	tac Tyr	cag Gln	atc Ile	cgc Arg	tac Tyr 200	cga Arg	gtg Val	gag Glu	gac Asp	agt Ser 205	gtg Val	gac Asp	tgg Trp	624
aag Lys	gtg Val 210	gtg Val	gac Asp	gat Asp	gtg Val	agc Ser 215	aac Asn	cag Gln	acc Thr	tcc Ser	tgc Cys 220	cgc Arg	ctg Leu	gcc Ala	ggc Gly	672
ctg Leu 225	aaa Lys	ccc Pro	ggc Gly	acc Thr	gtg Val 230	tac Tyr	ttc Phe	gtg Val	caa Gln	gtg Val 235	cgc Arg	tgc Cys	aac Asn	ccc Pro	ttt Phe 240	720
ggc Gly	atc Ile	tat Tyr	ggc Gly	tcc Ser 245	aag Lys	aaa Lys	gcc Ala	ggg Gly	atc Ile 250	tgg Trp	agt Ser	gag Glu	tgg Trp	agc Ser 255	cac His	768
ccc Pro	aca Thr	gcc Ala	gcc Ala 260	tcc Ser	act Thr	ccc Pro	cgc Arg	agt Ser 265	gag Glu	cgc Arg	ccg Pro	ggc Gly	ccg Pro 270	ggc Gly	ggc Gly	816
ggg Gly	gcg Ala	tgc Cys 275	gaa Glu	ccg Pro	cgg Arg	ggc Gly	gga Gly 280	gag Glu	ccg Pro	agc Ser	tcg Ser	ggg Gly 285	ccg Pro	gtg Val	cgg Arg	864
cgc Arg	gag Glu 290	ctc Leu	aag Lys	cag Gln	ttc Phe	ctg Leu 295	ggc Gly	tgg Trp	ctc Leu	aag Lys	aag Lys 300	cac His	gcg Ala	tac Tyr	tgc Cys	912

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tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga gcc tgg atg cag 960
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305 310 315 320

aag tcg cac aag acc cgc aac cag cac agg acg agg gga tcc tgc cct 1008
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
325 330 335

cgg gca gac ggg gca cgg cga gag gtc ctg cca gat aag ctg 1050
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
340 345 350

taggggctca ggccaccctc cctgccacgt ggagacgcag aggccgaacc caaactgggg 1110
ccacctctgt accctcactt cagggcacct gagcccctca gcaggagctg ggggtggcccc 1170
tgagctccaa cgcccataac agctctgact cccacgtgag gccacctttg ggtgcaccccc 1230
agtgggtgtg tgtgtgtgtg tgagggttgg ttgagttgcc tagaaccctt gccagggctg 1290
ggggtgagaa ggggagtcac tactcccat tacctagggc ccctccaaaa gagtcctttt 1350
aaataaatga gctatttagg tgcaaaaaaa aaaaaaaaaa a 1391

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<210> 25
 <211> 350
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Haemopoietin receptor

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<400> 25
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1 5 10 15

Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 20 25 30

Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 35 40 45

Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
 50 55 60

Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 65 70 75 80

Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
 85 90 95

Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
 100 105 110

Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
 115 120 125

Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
 130 135 140

Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
 19

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145		150		155		160									
Pro	Pro	Pro	Asp	Val ₁₆₅	His	Val	Ser	Arg	Val ₁₇₀	Gly	Gly	Leu	Glu	Asp ₁₇₅	Gln
Leu	Ser	Val	Arg ₁₈₀	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe ₁₉₀	Leu	Phe
Gln	Ala	Lys ₁₉₅	Tyr	Gln	Ile	Arg	Tyr ₂₀₀	Arg	Val	Glu	Asp	Ser ₂₀₅	Val	Asp	Trp
Lys	Val ₂₁₀	Val	Asp	Asp	Val	Ser ₂₁₅	Asn	Gln	Thr	Ser	Cys ₂₂₀	Arg	Leu	Ala	Gly
Leu	Lys	Pro	Gly	Thr	Val ₂₃₀	Tyr	Phe	Val	Gln	Val ₂₃₅	Arg	Cys	Asn	Pro	Phe ₂₄₀
Gly	Ile	Tyr	Gly	Ser ₂₄₅	Lys	Lys	Ala	Gly	Ile ₂₅₀	Trp	Ser	Glu	Trp	Ser ₂₅₅	His
Pro	Thr	Ala	Ala ₂₆₀	Ser	Thr	Pro	Arg	Ser ₂₆₅	Glu	Arg	Pro	Gly	Pro ₂₇₀	Gly	Gly
Gly	Ala	Cys ₂₇₅	Glu	Pro	Arg	Gly	Gly ₂₈₀	Glu	Pro	Ser	Ser	Gly ₂₈₅	Pro	Val	Arg
Arg	Glu ₂₉₀	Leu	Lys	Gln	Phe	Leu ₂₉₅	Gly	Trp	Leu	Lys	Lys ₃₀₀	His	Ala	Tyr	Cys
Ser	Asn	Leu	Ser	Phe	Arg ₃₁₀	Leu	Tyr	Asp	Gln	Trp ₃₁₅	Arg	Ala	Trp	Met	Gln ₃₂₀
Lys	Ser	His	Lys	Thr ₃₂₅	Arg	Asn	Gln	His	Arg ₃₃₀	Thr	Arg	Gly	Ser	Cys ₃₃₅	Pro
Arg	Ala	Asp	Gly ₃₄₀	Ala	Arg	Arg	Glu	Val ₃₄₅	Leu	Pro	Asp	Lys	Leu ₃₅₀		

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:UP1
 oligonucleotide

<400> 26
 tccaggcagc ggctcggggga caac

24

<210> 27
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:LP1
 oligonucleotide

<400> 27
 ttgctcacat cgccaccac cttc

24

<210> 28
<211> 6663
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: Murine NR6 gene

<400> 28
cccagaactc ttggacgctg aggcaggagg attcccaagt ttcaagacag tgtgttttcta 60
ggtaatgaga ccctgtcaag aaaagaaaag aaataaagag acaagaaaat gtttataggc 120
tgtgagacag cttggtgggt aaggggcact tgcctccaat caagatgacc tcagcccat 180
ccctaggaat ccatggtaga aggagaaagc aaactcgcag ctgctgacct ccatacatgt 240
gctccaatgt gcacacacac agggagacat aatcaattaa taggatgtat ttgcttagat 300
ttgagtaggc atttatgact gatgttttaa aatTTTTatt tgattttatg aaaatatacc 360
tgtttgtatt tggtttgggt tggtttgagt tttgtttatt tgagacaggg cttctctgtg 420
tagtcctggc tgtccttgga actcactctg tagaccaggc tggccttgaa ctcagaaatc 480
cgctgcttg tgcttcccaa gtgcttagat taaagggtgtg cactgccatt cagcaaaatt 540
gcatacttta accccagtat ttgggaggca gaggcagact aatgtgtgaa ttccaggcta 600
gccaaaggata cagagtgaga ccctattctt accctcccc cccaaaacc caaaatgtat 660
tttgtgcttg tgtatgtaca tgtgtgttgc agcacgtaaa tgtccaagga caacttgtag 720
aagttctctc cgttcacagt ctaagtcctg aattcaaact aaggctctca ggcttagcca 780
cagtcctctt tatgtactga gccatttcac tggccctgga ttgactgatg aattaatttt 840
tgagataagg tctcttgtag ctctagctag gctcaaacta tgaactcca aggtcatctt 900
gagctgctgg tactcttgct tccaccccaa gtggtggaat gatactcagg cagcacttct 960
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tctcgttggt tcttttcttt atctgtgaaa tgggtgaaca cctgttcaag acttcctgac 1080
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 Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser
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 ggggtggggg ga 11832

<210> 39

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Murine peptide

<400> 39

Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln
 1 5 10 15

Ala Thr Cys Ser Ile His Gly Asp Thr Pro
 20 25

<210> 40
 <211> 21
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 40
 gtccaagtgc gttgtaaccc a 21

<210> 41
 <211> 24
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 41
 gctgagtgtg cgctgggtct cacc 24

<210> 42
 <211> 18
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 42
 ggctccactc gtcacaga 18

<210> 43
 <211> 2079
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (513)..(1775)

<220>
 <223> Description of Unknown Organism: Nucleotide Sequence of NR6

<400> 43
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 tttttgaaag ctagctgact cactgttcaa gaaaggagaa cactttcaat tatgctgttt 120
 gactgcagtg tcagggatcc aaaggaaatg actccatccc ttccctttca tcccaacctc 180
 agtgacagca aattctgatg tgactgaggg ttggcttgtg aaggagtcac taggaaattc 240
 tgcctaagcc atagcgcgat gagaaggatg taccctatgg tgggtgatttt cctgtgcccc 300
 ctcagaggaa agttgtcaga tgagcaggtg gagtattcta tagcaaacag caagctaata 360

ggttacacag ataactctct gactttgcct tacagaacct gtgctattga ccttagggca	420
aggttcatgc tcagggggcc aactctgtgg gttaggattt gagtttaagc agcttctgct	480
catatttcag cgccccggc agcgccggcc cc atg ccc gcc ggc cgc cgg ggc	533
Met Pro Ala Gly Arg Arg Gly	
1 5	
ccc gcc gcc caa tcc gcg cgg cgg ccg ccg ccg ttg ctg ccc ctg ctg	581
Pro Ala Ala Gln Ser Ala Arg Arg Pro Pro Pro Leu Leu Pro Leu Leu	
10 15 20	
ctg ctc tgc gtc ctc ggg gcg ccg cga gcc gga tca gga gcc cac aca	629
Leu Leu Cys Val Leu Gly Ala Pro Arg Ala Gly Ser Gly Ala His Thr	
25 30 35	
gct gtg atc agt ccc cag gat ccc acg ctt ctc atc ggc tcc tcc ctg	677
Ala Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu	
40 45 50 55	
ctg gcc acc tgc tca gtg cac gga gac cca cca gga gcc acc gcc gag	725
Leu Ala Thr Cys Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu	
60 65 70	
ggc ctc tac tgg acc ctc aat ggg cgc cgc ctg ccc cct gag ctc tcc	773
Gly Leu Tyr Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser	
75 80 85	
cgt gta ctc aac gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat	821
Arg Val Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn	
90 95 100	
ggg tcc agg cag cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac	869
Gly Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp	
105 110 115	
ggc agc atc ctg gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag	917
Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu	
120 125 130 135	
aaa ccc gtc aac atc agc tgc tgg tcc aag aac atg aag gac ttg acc	965
Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr	
140 145 150	
tgc cgc tgg acg cca ggg gcc cac ggg gag acc ttc ctc cac acc aac	1013
Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn	
155 160 165	
tac tcc ctc aag tac aag ctt agg tgg tat ggc cag gac aac aca tgt	1061

Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys		
		170					175					180					
gag	gag	tac	cac	aca	gtg	ggg	ccc	cac	tcc	tgc	cac	atc	ccc	aag	gac	1109	
Glu	Glu	Tyr	His	Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp		
	185					190					195						
ctg	gct	ctc	ttt	acg	ccc	tat	gag	atc	tgg	gtg	gag	gcc	acc	aac	cgc	1157	
Leu	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg		
200					205					210					215		
ctg	ggc	tct	gcc	cgc	tcc	gat	gta	ctc	acg	ctg	gat	atc	ctg	gat	gtg	1205	
Leu	Gly	Ser	Ala	Arg	Ser	Asp	Val	Leu	Thr	Leu	Asp	Ile	Leu	Asp	Val		
				220					225					230			
gtg	acc	acg	gac	ccc	ccg	ccc	gac	gtg	cac	gtg	agc	cgc	gtc	ggg	ggc	1253	
Val	Thr	Thr	Asp	Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly		
			235					240					245				
ctg	gag	gac	cag	ctg	agc	gtg	cgc	tgg	gtg	tcg	cca	ccc	gcc	ctc	aag	1301	
Leu	Glu	Asp	Gln	Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys		
		250					255					260					
gat	ttc	ctc	ttt	caa	gcc	aaa	tac	cag	atc	cgc	tac	cga	gtg	gag	gac	1349	
Asp	Phe	Leu	Phe	Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp		
	265					270					275						
agt	gtg	gac	tgg	aag	gtg	gtg	gac	gat	gtg	agc	aac	cag	acc	tcc	tgc	1397	
Ser	Val	Asp	Trp	Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys		
280					285					290					295		
cgc	ctg	gcc	ggc	ctg	aaa	ccc	ggc	acc	gtg	tac	ttc	gtg	caa	gtg	cgc	1445	
Arg	Leu	Ala	Gly	Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg		
				300					305					310			
tgc	aac	ccc	ttt	ggc	atc	tat	ggc	tcc	aag	aaa	gcc	ggg	atc	tgg	agt	1493	
Cys	Asn	Pro	Phe	Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser		
			315					320					325				
gag	tgg	agc	cac	ccc	aca	gcc	gcc	tcc	act	ccc	cgc	agt	gag	cgc	ccg	1541	
Glu	Trp	Ser	His	Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro		
		330					335					340					
ggc	ccg	ggc	ggc	ggg	gcg	tgc	gaa	ccg	cgg	ggc	gga	gag	ccg	agc	tcg	1589	
Gly	Pro	Gly	Gly	Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser		
	345					350					355						
ggg	ccg	gtg	cgg	cgc	gag	ctc	aag	cag	ttc	ctg	ggc	tgg	ctc	aag	aag	1637	
Gly	Pro	Val	Arg	Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys		
360					365					370					375		
cac	gcg	tac	tgc	tcc	aac	ctc	agc	ttc	cgc	ctc	tac	gac	cag	tgg	cga	1685	

His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg
 380 385 390
 gcc tgg atg cag aag tcg cac aag acc cgc aac cag gac gag ggg atc 1733
 Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile
 395 400 405
 ctg ccc tcg ggc aga cgg ggc acg gcg aga ggt cct gcc aga 1775
 Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro Ala Arg
 410 415 420
 taagctgtag gggctcaggc caccctccct gccacgtgga gacgcagagg ccgaacccaa 1835
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 gtgcacccca gtgggtgtgt gtgtgtgtgt gagggttggt tgagttgcct agaaccctg 2015
 ccagggctgg ggggtgagaag gggagtcatt actccccatt acctagggcc cctccaaaag 2075
 atcc 2079

<210> 44
 <211> 421
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Amino Acid Sequence of NR6

<400> 44
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 Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly Ala Pro Arg
 20 25 30
 Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro Gln Asp Pro Thr
 35 40 45
 Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys Ser Val His Gly Asp
 50 55 60
 Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn Gly Arg
 65 70 75 80
 Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn Ala Ser Thr Leu Ala
 85 90 95
 Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Arg Ser Gly Asp Asn
 100 105 110
 Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser Cys Leu
 115 120 125

Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn Ile Ser Cys Trp Ser
 130 135 140
 Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly
 145 150 155 160
 Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp
 165 170 175
 Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His
 180 185 190
 Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile
 195 200 205
 Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
 210 215 220
 Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp Val
 225 230 235 240
 His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val Arg Trp
 245 250 255
 Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys Tyr Gln
 260 265 270
 Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val Asp Asp
 275 280 285
 Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro Gly Thr
 290 295 300
 Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr Gly Ser
 305 310 315 320
 Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala Ala Ser
 325 330 335
 Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Ala Cys Glu Pro
 340 345 350
 Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu Lys Gln
 355 360 365
 Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu Ser Phe
 370 375 380
 Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr
 385 390 395 400
 Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala
 405 410 415
 Arg Gly Pro Ala Arg
 420

<210> 45
 <211> 23
 <212> DNA
 <213> Artificial
 <220>

<223> Description of Artificial Sequence: Fwd Primer

<400> 45
tgccccaga gaaacccgtc aac 23

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Rev Primer

<400> 46
cgtgagtaca tcggagcggg cagag 25

<210> 47
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 47
tcaggcgcgc cttgccaca cagctgtgat c 31

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 48
tcaggcgcgc ccttatctgg caggacctct 30

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 49
tcaggcgcgc ctgcccgcgc gccgc 25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: oligonucleotide
 <400> 50
 ataaggcgcg ccctggcagg acctctcg 28

<210> 51
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: oligonucleotide
 <400> 51
 tcaggcgcg cttgccaca cagctgtgat c 31

<210> 52
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: oligonucleotide
 <400> 52
 tcaggcgcg ccttatctgg caggacctct 30

<210> 53
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: oligonucleotide
 <400> 53
 tcaggcgcg ctgcccgcg gccgc 25

<210> 54
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: oligonucleotide
 <400> 54
 ataaggcgcg ccctggcagg acctctcg 28

<210> 55
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide

<400> 55

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 56
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 56
ctagactagt gctgacacaa tggttcttgc cagctctacc accagcatcc acaccatgct 60
gctcctgctc ctgatgctct tccacctggg actccaagct tcaatctcgg cgcgccagga 120
ctacaaggac gacgatgaca agacgcgtgc tagcactagt 160

<210> 57
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 58
aataaataaa 10